SEQUENCE LISTING

<110> Maeda, Masatsugu
Yaguchi, Noriko

<120> NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR10

<130> 06501-096001

<140> US 10/006,265
<141> 2001-12-03

<150> PCT/JP00/03556
<151> 2000-06-01

<150> JP 11/155797
<151> 1999-06-02

<150> JP 11/217797
<151> 1999-07-30

<160> 40

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 2969
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (523)...(2478)

<400> 1
cgcttataaa tgaatgtgtg cttaggaaca ccagacagca ctccagcact ctgcttgggg 60
ggcattcgaa acagcaaaat cactcataaa aggcaaaaaa ttgcaaaaaa aatagtaata 120
accagcatgg tactaaatag accatgaaaa gacatgtgtg tgcagtatga aaattgagac 180
aggaaggcag agtgtcagct tgttccacct cagctgggaa tgtgcatcag gcaactcaag 240
tttttcacca cggcatgtgt ctgtgaatgt ccgcaaaaca ttttaacaat aatgcaatcc 300
atttcccagc ataagtgggt aagtgccact ttgacttggg ctgggcttaa aagcacaaga 360
aaagctcgca gacaatcaga gtggaaacac tcccacatct tagtgtggat aaattaaagt 420
ccagattgtt cttcctgtcc tgacttgtgc tgtgggaggt ggagttgcct ttgatgcaaa 480
tcctttgagc cagcagaaca tctgtggaac atcccctgat ac atg aag ctc tct 534
Met Lys Leu Ser
1

ccc cag cct tca tgt gtt aac ctg ggg atg atg tgg acc tgg gca ctg 582
Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp Thr Trp Ala Leu
5 10 15 20

tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg cca gct 630
Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu Pro Ala
25 30 35

aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat tta acc 678

```
Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn Leu Thr
            40                  45                  50

tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac aca gtt      726
Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr Thr Val
         55                  60                  65

aag aga act tac gct ttc gga gaa aaa cat gat aat tgt aca acc aat      774
Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr Thr Asn
     70                  75                  80

agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt cca aga      822
Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu Pro Arg
 85                  90                  95                 100

ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa aat gga      870
Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu Asn Gly
                105                 110                 115

gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag aac ata      918
Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu Asn Ile
            120                 125                 130

gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt ttg ggc      966
Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val Leu Gly
        135                 140                 145

atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg gcg cct     1014
Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu Ala Pro
    150                 155                 160

gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc aac agt     1062
Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val Asn Ser
165                 170                 175                 180

acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat aaa aac     1110
Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn
                185                 190                 195

caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat gtc ata     1158
Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr Val Ile
            200                 205                 210

gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac tgg agc     1206
Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser
        215                 220                 225

caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc ctg gaa     1254
Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro Cys Gly Leu Glu
    230                 235                 240

ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg cca gtg     1302
Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg Pro Val
245                 250                 255                 260

cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag aaa aca     1350
Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu Lys Thr
```

```
                265                 270                 275

ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac ctc aca     1398
Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn Leu Thr
            280                 285                 290

gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg gga ggc     1446
Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu Gly Gly
        295                 300                 305

gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg aag tct     1494
Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly Lys Ser
    310                 315                 320

cca gtg gcc acc ctg agg att cca gct att caa gaa aaa tca ttt cag     1542
Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys Ser Phe Gln
325                 330                 335                 340

tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta gtg gtg     1590
Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu Val Val
                345                 350                 355

aag tgg caa agc tct gct cta gac gtg aac act tgg atg att gaa tgg     1638
Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile Glu Trp
            360                 365                 370

ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa tct gtg     1686
Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu Ser Val
        375                 380                 385

tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa cct ttc     1734
Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys Pro Phe
    390                 395                 400

tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa gtt ggc     1782
Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys Val Gly
405                 410                 415                 420

gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca tca gaa     1830
Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro Ser Glu
                425                 430                 435

ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc acg atc     1878
Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val Thr Ile
            440                 445                 450

aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc tgc aac     1926
Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile Cys Asn
        455                 460                 465

tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc aag aca     1974
Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser Lys Thr
    470                 475                 480

gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa cga aag     2022
Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys Arg Lys
485                 490                 495                 500
```

```
acc tct tac att gtt cag gtc atg gcc aac acc agt gct ggg gga acc     2070
Thr Ser Tyr Ile Val Gln Val Met Ala Asn Thr Ser Ala Gly Gly Thr
                505                 510                 515

aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc ttt gag     2118
Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val Phe Glu
            520                 525                 530

att atc ctc ata act tct ctg att ggt gga ggc ctt ctt att ctc att     2166
Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu Leu Ile Leu Ile
        535                 540                 545

atc ctg aca gtg gca tat ggt ctc aaa aaa ccc aac aaa ttg act cat     2214
Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu Thr His
    550                 555                 560

ctg tgt tgg ccc acc gtt ccc aac cct gct gaa agt agt ata gcc aca     2262
Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile Ala Thr
565                 570                 575                 580

tgg cat gga gat gat ttc aag gat aag cta aac ctg aag gag tct gat     2310
Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu Ser Asp
                585                 590                 595

gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc acc ccc     2358
Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser Thr Pro
            600                 605                 610

agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg aat gtt     2406
Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly Asn Val
        615                 620                 625

ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa aaa caa     2454
Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu Lys Gln
    630                 635                 640

ttt agg agg gga aaa gaa tgg gac tagaattctg tcttcctgcc caacttcaat    2508
Phe Arg Arg Gly Lys Glu Trp Asp
645                 650

ataagtgtgg actaaaatgc gagaaaggtg tcctgtggtc tatgcaaatt agaaaggaca   2568
tgcagagttt tccaactagg aagactgaat ctgtggcccc aagagaacca tctccgaaga   2628
ctgggtatgt ggtcttttcc acacatggac cacctacgga tgcaatctgt aatgcatgtg   2688
catgagaagt ctgttattaa gtagagtgtg aaaacatggt tatggtaata ggaacagctt   2748
ttaaaatgct tttgtatttg ggcctttcac acaaaaaagc cataatacca ttttcatgta   2808
atgctatact tctatactat tttcatgtaa tactatactt ctatactatt ttcatgtaat   2868
actatacttc tatactattt tcatgtaata ctatacttct atattaaagt tttacccact   2928
ccaaaaaaag aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a                       2969

<210> 2
<211> 652
<212> PRT
<213> Homo sapiens

<400> 2
Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
```

```
 1               5                  10                  15
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
            20                  25                  30
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
            100                 105                 110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
225                 230                 235                 240
Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly
                245                 250                 255
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
            260                 265                 270
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn
        275                 280                 285
Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
    290                 295                 300
His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
305                 310                 315                 320
Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
                325                 330                 335
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
            340                 345                 350
Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
        355                 360                 365
Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
    370                 375                 380
Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
385                 390                 395                 400
Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
                405                 410                 415
Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
            420                 425                 430
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
        435                 440                 445
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
    450                 455                 460
```

```
Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
465                 470                 475                 480
Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
                485                 490                 495
Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Asn Thr Ser
            500                 505                 510
Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
        515                 520                 525
Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
    530                 535                 540
Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
545                 550                 555                 560
Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
                565                 570                 575
Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
            580                 585                 590
Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
        595                 600                 605
Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
    610                 615                 620
Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
625                 630                 635                 640
Gln Glu Lys Gln Phe Arg Arg Gly Lys Glu Trp Asp
                645                 650
```

<210> 3
<211> 2440
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (523)...(1278)

<400> 3

```
cgcttataaa tgaatgtgtg cttaggaaca ccagacagca ctccagcact ctgcttgggg     60
ggcattcgaa acagcaaaat cactcataaa aggcaaaaaa ttgcaaaaaa aatagtaata    120
accagcatgg tactaaatag accatgaaaa gacatgtgtg tgcagtatga aaattgagac    180
aggaaggcag agtgtcagct tgttccacct cagctgggaa tgtgcatcag gcaactcaag    240
tttttcacca cggcatgtgt ctgtgaatgt ccgcaaaaca ttttaacaat aatgcaatcc    300
atttcccagc ataagtgggt aagtgccact ttgacttggg ctgggcttaa aagcacaaga    360
aaagctcgca gacaatcaga gtggaaacac tcccacatct tagtgtggat aaattaaagt    420
ccagattgtt cttcctgtcc tgacttgtgc tgtgggaggt ggagttgcct ttgatgcaaa    480
tcctttgagc cagcagaaca tctgtggaac atcccctgat ac atg aag ctc tct       534
                                              Met Lys Leu Ser
                                               1

ccc cag cct tca tgt gtt aac ctg ggg atg atg tgg acc tgg gca ctg       582
Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp Thr Trp Ala Leu
 5                  10                  15                  20

tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg cca gct       630
Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu Pro Ala
                25                  30                  35

aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat tta acc       678
Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn Leu Thr
```

```
                40                  45                  50

tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac aca gtt      726
Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr Thr Val
         55                  60                  65

aag aga act tac gct ttc gga gaa aaa cat gat aat tgt aca acc aat      774
Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr Thr Asn
     70                  75                  80

agt tct aca agt gaa aat cgt gct tcg tgc tct ttt ttc ctt cca aga      822
Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu Pro Arg
 85                  90                  95                 100

ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa aat gga      870
Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu Asn Gly
                105                 110                 115

gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag aac ata      918
Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu Asn Ile
            120                 125                 130

gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt ttg ggc      966
Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val Leu Gly
        135                 140                 145

atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg gcg cct     1014
Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu Ala Pro
    150                 155                 160

gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc aac agt     1062
Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val Asn Ser
165                 170                 175                 180

acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat aaa aac     1110
Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn
                185                 190                 195

caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat gtc ata     1158
Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr Val Ile
            200                 205                 210

gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac tgg agc     1206
Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser
        215                 220                 225

caa gaa aaa atg gga atg act gag gaa gaa ggc aag cta ctc cct gcg     1254
Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys Leu Leu Pro Ala
    230                 235                 240

att ccc gtc ctg tct act ctg gtg tagggctgct ttgggctaga cttggtgggg    1308
Ile Pro Val Leu Ser Thr Leu Val
245                 250

tttgtcacca cctggttggg aatcatggaa tctcatgacc ccaggggccc cctgtaccat   1368
cgagagtgag cctgcacaac tttgtgcccc aaaggcaaag gatcacattt taatactcat   1428
gaggttctta tactatacat gaaagggtat catatcattt gttttgtttt gttttgtttt   1488
```

```
tgagatggag tcttactctg tcacccagga tggagtgcag tgatgtgatc tcggctcact   1548
gccaccacca cctcccgagt tcaagcaatt cttgtgcctc agcctcccaa gtagctggga   1608
ttacaggggc ccacgaccat gcccggttga tttttgtatt tttagtagag aagggatatc   1668
accatgttgg ctaggctagt cttgaactcc tgacctcagg taatctgccc accttgacct   1728
cccaaagtgt tgggattaca ggcgtgagcc actgtgcccc gccagtatca tatcatctga   1788
aggtatcctg tgataaatta aagatacata ttgtgaatcc tggagctact actcaaaaaa   1848
taaataaagg tgtaactaat acaatttaaa aaatcacatt tttaatgaca gtgaggaaag   1908
gaaagaggca tggattgcag gttgatggag tgcttactaa gtgtcagtat ggtcattaag   1968
agcaacgctt ccagtcagtg gccttggctt aaatcccaag ccaggtgtct ttgggcaaga   2028
tacctaaact ctcagttcat tctcagcagt ttcctcgcat ttattccct tttctatatt   2088
gaaatagaat atgtaagttg agtttatagt agtacctatt ttttagtatt attttaaaga   2148
ttaaatgaaa taatgtgttt agcccatagt agatattcac taactgctag acttcctatt   2208
cttattattt atcctcctac tattattttt aatcctcctt aaagcactat aaaatatgta   2268
gagtcactcc cattttggaa atgaggaaac tgagtttcag agatgctaat aaacagctca   2328
gggtcactca gcatgtgtta cttttctcaa gagccttgcc cagagtctga ccctcagtgg   2388
acgatcaata aatgtgtgat gaatggaaaa aaaaaaaaaa aaaaaaaaaa aa            2440
```

<210> 4
<211> 252
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
 1               5                  10                  15
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
            20                  25                  30
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
            100                 105                 110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys
225                 230                 235                 240
Leu Leu Pro Ala Ile Pro Val Leu Ser Thr Leu Val
                245                 250
```

<210> 5

<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5
atggaagtca acttcgctaa gaaccgtaag 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
ccaaacgtac aacctcacgg ggctgcaacc 30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

Q1
<220>
<223> primer

<400> 7
gtcatagctc tgcgatgtgc ggtcaaggag 30

<210> 8
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 8
agtagcttgc gttcttcctc agctattccc 30

<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 9
ctttgactcc ttgaccgcac atcgcagagc 30

<210> 10
<211> 30
<212> DNA

<213> Artificial Sequence

<220>
<223> primer

<400> 10
ggttgcagcc ccgtgaggtt gtacgtttgg 30

<210> 11
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
atcagatgaa acaggcgcca actcagg 27

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 12
tggtttcaca cggaaaatct taggtgg 27

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
gcattcagga cagtcaacag taccagc 27

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
agctggaatc ctcagggtgg ccactgg 27

<210> 15
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
gcccatcacc agagtagaca ggacggg 27

<210> 16
<211> 2119
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (11)...(1996)

<400> 16
```
ccctgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg ggg        49
            Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly
             1               5                  10

atg atg tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc       97
Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe
     15                  20                  25

agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac      145
Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr
 30                  35                  40                  45

tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc      193
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr
                 50                  55                  60

agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa      241
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
             65                  70                  75

cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg      289
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
         80                  85                  90

tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att      337
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
     95                  100                 105

gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca      385
Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
110                 115                 120                 125

tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc      433
Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
                130                 135                 140

cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg      481
Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
            145                 150                 155

ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt      529
```

```
Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
        160                 165                 170

cga ttc agg aca gtc aac agt acc agc tgg atg gaa gtc aac ttc gct      577
Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
    175                 180                 185

aag aac cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg cag      625
Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
190                 195                 200                 205

cct ttt aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca      673
Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
                210                 215                 220

aag ttc tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa      721
Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
            225                 230                 235

gaa gct cca tgt ggc ctg gaa ctg tgg aga gtc ctg aaa cca gct gag      769
Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
        240                 245                 250

gcg gat gga aga agg cca gtg cgg ttg tta tgg aag aag gca aga gga      817
Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
    255                 260                 265

gcc cca gtc cta gag aaa aca ctt ggc tac aac ata tgg tac tat cca      865
Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
270                 275                 280                 285

gaa agc aac act aac ctc aca gaa aca atg aac act act aac cag cag      913
Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
                290                 295                 300

ctt gaa ctg cat ctg gga ggc gag agc ttt tgg gtg tct atg att tct      961
Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
            305                 310                 315

tat aat tct ctt ggg aag tct cca gtg gcc acc ctg agg att cca gct     1009
Tyr Asn Ser Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala
        320                 325                 330

att caa gaa aaa tca ttt cag tgc att gag gtc atg cag gcc tgc gtt     1057
Ile Gln Glu Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val
    335                 340                 345

gct gag gac cag cta gtg gtg aag tgg caa agc tct gct cta gac gtg     1105
Ala Glu Asp Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val
350                 355                 360                 365

aac act tgg atg att gaa tgg ttt ccg gat gtg gac tca gag ccc acc     1153
Asn Thr Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr
                370                 375                 380

acc ctt tcc tgg gaa tct gtg tct cag gcc acg aac tgg acg atc cag     1201
Thr Leu Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln
```

```
            385                 390                 395

caa gat aaa tta aaa cct ttc tgg tgc tat aac atc tct gtg tat cca     1249
Gln Asp Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro
        400                 405                 410

atg ttg cat gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc     1297
Met Leu His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala
    415                 420                 425

aaa gaa ggc gtt cca tca gaa ggt cct gag acc aag gtg gag aac att     1345
Lys Glu Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile
430                 435                 440                 445

ggc gtg aag acg gtc acg atc aca tgg aaa gag att ccc aag agt gag     1393
Gly Val Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu
                450                 455                 460

aga aag ggt atc atc tgc aac tac acc atc ttt tac caa gct gaa ggt     1441
Arg Lys Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly
            465                 470                 475

gga aaa gga ttc tcc aag aca gtc aat tcc agc atc ttg cag tac ggc     1489
Gly Lys Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly
        480                 485                 490

ctg gag tcc ctg aaa cga aag acc tct tac att gtt cag gtc atg gcc     1537
Leu Glu Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala
    495                 500                 505

agc acc agt gct ggg gga acc aac ggg acc agc ata aat ttc aag aca     1585
Ser Thr Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr
510                 515                 520                 525

ttg tca ttc agt gtc ttt gag att atc ctc ata act tct ctg att ggt     1633
Leu Ser Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly
                530                 535                 540

gga ggc ctt ctt att ctc att atc ctg aca gtg gca tat ggt ctc aaa     1681
Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys
            545                 550                 555

aaa ccc aac aaa ttg act cat ctg tgt tgg ccc acc gtt ccc aac cct     1729
Lys Pro Asn Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro
        560                 565                 570

gct gaa agt agt ata gcc aca tgg cat gga gat gat ttc aag gat aag     1777
Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys
    575                 580                 585

cta aac ctg aag gag tct gat gac tct gtg aac aca gaa gac agg atc     1825
Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile
590                 595                 600                 605

tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag ttg     1873
Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu
                610                 615                 620
```

```
gtg gtg aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa gcc     1921
Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala
            625                 630                 635

aga acg ggt cag gaa aac aat tta gga ggg gaa aag aat ggg act aga     1969
Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg
        640                 645                 650

att ctg tct tcc tgc cca act tca ata taagtgtgga ctaaaatgcg           2016
Ile Leu Ser Ser Cys Pro Thr Ser Ile
    655                 660

agaaaggtgt cctgtggtct atgcaaatta gaaaggacat gcagagtttt ccaactagga   2076
agactgaatc tgtggcccca agagaaccat ctccgaagac tgg                     2119

<210> 17
<211> 662
<212> PRT
<213> Homo sapiens

<400> 17
Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp
 1               5                  10                  15
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
            20                  25                  30
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
        35                  40                  45
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
    50                  55                  60
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65                  70                  75                  80
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
                85                  90                  95
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
            100                 105                 110
Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg
        115                 120                 125
Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys
    130                 135                 140
Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro
145                 150                 155                 160
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg
                165                 170                 175
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg
            180                 185                 190
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr
        195                 200                 205
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp
    210                 215                 220
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro
225                 230                 235                 240
Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly
                245                 250                 255
Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
            260                 265                 270
Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn
```

```
        275                 280                 285
Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu
    290                 295                 300
His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser
305                 310                 315                 320
Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu
                325                 330                 335
Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp
            340                 345                 350
Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp
        355                 360                 365
Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser
    370                 375                 380
Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys
385                 390                 395                 400
Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His
                405                 410                 415
Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly
            420                 425                 430
Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys
        435                 440                 445
Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly
    450                 455                 460
Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly
465                 470                 475                 480
Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser
                485                 490                 495
Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser
            500                 505                 510
Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe
        515                 520                 525
Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu
    530                 535                 540
Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn
545                 550                 555                 560
Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser
                565                 570                 575
Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu
            580                 585                 590
Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro
        595                 600                 605
Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn
    610                 615                 620
Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly
625                 630                 635                 640
Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser
                645                 650                 655
Ser Cys Pro Thr Ser Ile
            660
```

<210> 18
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
cccctgatac atgaagctct ctccccagcc 30

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
ccagtcttcg gagatggttc tcttggggcc 30

<210> 20
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
ctgtgtaagt accaattgtt cccaggc 27

<210> 21
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> misc_feature
<222> 7-9
<223> n = a, t, g, or c

<400> 21
tggagynnnt ggagy 15

<210> 22
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 3
<223> Xaa = any amino acid

<400> 22
Trp Ser Xaa Trp Ser
1 5

<210> 23
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 23
Tyr Thr Val Gln Val Arg
1 5

<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 24
Tyr Glu Ala Arg Val Arg
1 5

<210> 25
<211> 6
<212> PRT
<213> Artificial Sequence

R1

<220>
<223> exemplary motif

<400> 25
Tyr Ser Leu Gln Leu Arg
1 5

<210> 26
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 3-8
<223> Xaa = any amino acid

<400> 26
Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr
1 5 10

<210> 27
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 3-8
<223> Xaa = any amino acid

<400> 27
Val Gln Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr
 1   5   10

<210> 28
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<221> VARIANT
<222> 3-8
<223> Xaa = any amino acid

<400> 28
Cys Lys Xaa Xaa Xaa Xaa Xaa Xaa Gly Ile
 1   5   10

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 29
Trp Ser Glu Trp Ser Pro
 1   5

<210> 30
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 30
Trp Ser Asp Trp Ser Glu
 1   5

<210> 31
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 31
Trp Ser Pro Trp Ser Gln
 1   5

<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 32
Tyr Val Ile Ala Leu Arg
 1   5

<210> 33
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> exemplary motif

<400> 33
Trp Ser Asp Trp Ser
 1   5

Q1

<210> 34
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (211)...(399)

<221> misc_feature
<222> 281, 376, 420
<223> n = A,T,C or G

<400> 34
ttggtggttc atggtgatgt tctatatctg tgtaagtacc aattgttccc aggcacatat 60
ggaagtctgt taataaaaat gatatatttt aaaatttgat ttagagtgtt actagttcta 120
aaaatgtaaa agtacactag gtagtgaaga ggaaaatggg aggataacgt gtggtctcca 180
tttcagttta cgattgtctc tgtcttgtag atg gaa gtc aac ttc gct aag aac 234
                                Met Glu Val Asn Phe Ala Lys Asn
                                 1   5

cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg caa cct tnt 282
Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Xaa
     10   15   20

aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc 330
Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe

```
 25                  30                  35                  40

tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa gaa ngc      378
Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Xaa
                 45                  50                  55

aag cta ctt cct gcg att ccc gtcctgtctg ctctggtgta nggctgctct        429
Lys Leu Leu Pro Ala Ile Pro
             60

gcgctaaact tggtggtgtc tgcaccaccg                                   459

<210> 35
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> 24, 54
<223> Xaa = any amino acid

<400> 35
Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr
 1               5                  10                  15
Asn Leu Thr Gly Leu Gln Pro Xaa Thr Glu Tyr Val Ile Ala Leu Arg
            20                  25                  30
Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys
        35                  40                  45
Met Gly Met Thr Glu Glu Glu Xaa Lys Leu Leu Pro Ala Ile Pro
    50                  55                  60

<210> 36
<211> 42
<212> PRT
<213> Homo sapiens

<400> 36
Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg
 1               5                  10                  15
Ile Arg Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser
            20                  25                  30
Glu Glu Ala Ser Gly Ile Thr Tyr Glu Asp
        35                  40

<210> 37
<211> 37
<212> PRT
<213> Homo sapiens

<400> 37
Leu Asp Lys Leu Asn Pro Tyr Thr Leu Tyr Thr Phe Arg Ile Arg Cys
 1               5                  10                  15
Ser Thr Glu Thr Phe Trp Lys Trp Ser Lys Trp Ser Asn Lys Lys Gln
            20                  25                  30
His Leu Thr Thr Glu
        35
```

<210> 38
<211> 42
<212> PRT
<213> Homo sapiens

<400> 38
Asn Gly Glu Tyr Phe Leu Ser Glu Leu Glu Pro Ala Thr Glu Tyr Met
1 5 10 15
Ala Arg Val Arg Cys Ala Asp Ala Ser His Phe Trp Lys Trp Ser Glu
20 25 30
Trp Ser Gly Gln Asn Phe Thr Thr Leu Glu
35 40

<210> 39
<211> 45
<212> PRT
<213> Homo sapiens

<400> 39
Ala Lys Gly Arg His Asp Leu Leu Asp Leu Lys Pro Phe Thr Glu Tyr
1 5 10 15
Glu Phe Gln Ile Ser Ser Lys Leu His Leu Tyr Lys Gly Ser Trp Ser
20 25 30
Asp Trp Ser Glu Ser Leu Arg Ala Gln Thr Pro Glu Glu
35 40 45

<210> 40
<211> 51
<212> PRT
<213> Homo sapiens

<400> 40
Asn Gln Thr Ser Cys Arg Leu Ala Gly Leu Lys Pro Gly Thr Val Tyr
1 5 10 15
Phe Val Gln Val Arg Cys Asn Pro Phe Gly Ile Tyr Gly Ser Lys Lys
20 25 30
Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala Ala Ser Thr Pro
35 40 45
Arg Ser Gly
50